Raw Sequence Listing Error Summary

$H2$???
Bill
3 ???

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/093,992B_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ___ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ___ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ___ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ___ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ___ Variable Length
Sequence(s) ___ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 ___ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 ___ Skipped Sequences (OLD RULES)
Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ___ Skipped Sequences (NEW RULES)
Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ___ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ___ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ___ Use of <220>Feature (NEW RULES)
Sequence(s) ___ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 ___ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

```
         RAW SEQUENCE LISTING              DATE: 03/23/2001
         PATENT APPLICATION: US/09/093,972B   TIME: 12:55:56

         Input Set : A:\ES.txt
         Output Set: N:\CRF3\03232001\I093972B.raw
```

Does Not Comply
Corrected Diskette Needed

```
              SEQUENCE LISTING
   3 (1) GENERAL INFORMATION:
   4      (i) APPLICANT: Nyce, Jonathan W.
   5     (ii) TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
   6                              & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED
   7                              WITH BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
E--> 8    (iii) NUMBER OF SEQUENCES: (966)
   9     (iv) CORRESPONDENCE ADDRESS:
  10          (A) ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
  11          (B) STREET: 7 Clarke Drive
  12          (C) CITY: Cranbury
  13          (D) STATE: New Jersey
  14          (E) COUNTRY: USA
  15          (F) ZIP: 08512
  16      (v) COMPUTER READABLE FORM:
  17          (A) MEDIUM TYPE: Floppy disk
  18          (B) COMPUTER: IBM PC compatible
  19          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  20          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  21     (vi) CURRENT APPLICATION DATA:
  34          (A) APPLICATION NUMBER: US/09/093,972B
  35          (B) FILING DATE: 09-Jun-1998
  36          (C) CLASSIFICATION:
  37    (viii) ATTORNEY/AGENT INFORMATION:
  38          (A) NAME: Amzel, Viviana
  39          (B) REGISTRATION NUMBER: 30,930
C--> 40          (C) REFERENCE/DOCKET NUMBER: EPI-00672
  41                                        (D)
  42     (ix) TELECOMMUNICATION INFORMATION:
  43          (A) TELEPHONE: 609-409-3035
  44          (B) TELEFAX: 413-254-9245
  45          (C) TELEX:
```

Handwritten annotations: "996 in file (next page)"; "pp 1-4"; "OK"; "see page 4"

ERRORED SEQUENCES

```
9891 (2) INFORMATION FOR SEQ ID NO: 984:
9892      (i) SEQUENCE CHARACTERISTICS:
9893          (A) LENGTH: 24 base pairs
9894          (B) TYPE: nucleic acid
9895          (C) STRANDEDNESS: single
9896          (D) TOPOLOGY: linear
9897     (ii) MOLECULE TYPE: DNA (genomic)
9898     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984:
E--> 9899  5?-CCG CGC CTC CGC CTG CCG CTT CTG                24
```

Handwritten annotation: "delete - do not show prime marks in the sequence itself"

(2) INFORMATION FOR SEQ ID NO:996:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:
TTT CTT CTG TTC CC
14

last sequence in file

format err - see item 1 on Error Summary Sheet

(1) delete at end of file

(Uii) ~~(vi)~~ PRIOR (PRIORITY) APPLICATION DATA:
   (A) APPLICATION NUMBER: US 08/472,527
   (B) FILING DATE: 7-June-1995
(Uii) ~~(vi)~~ (PRIORITY) APPLICATION DATA:
       PRIOR

edit all entries — These are samples

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Amzel, Viviana
(B) REGISTRATION NUMBER: 30,930
(C) REFERENCE/DOCKET NUMBER: EPI-00672
(D) *delete* REFERENCE/DOCKET NUMBER:

VERIFICATION SUMMARY   DATE: 03/23/2001
PATENT APPLICATION: US/09/093,972B   TIME: 12:55:59

Input Set : A:\ES.txt
Output Set: N:\CRF3\03232001\I093972B.raw

```
L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:40 M:220 C: Keyword misspelled or invalid format, [(C) REFERENCE/DOCKET NUMBER:]
L:9899 M:254 E: No. of Bases conflict, Input:24 Counted:24 SEQ:984
L:9899 M:320 E: (1) Wrong Nucleic Acid Designator, 3
L:9899 M:204 E: No. of Bases differ, LENGTH:Input:24 Counted:26 SEQ:984
L:10021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:996
L:8 M:203 E: No. of Seq. differs, : Input 966, Counted 996
```